

10/517420

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SEQUENCE LISTING

<110> CABEZON SILIVA, Teresa Elisa Virginia
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VINALS Y DE BASSOLS, Carlota

<120> Immunogenic Compositions

<130> B45311

<140> To Be Assigned

<150> PCT/EP03/06096

<151> 2003-06-06

<150> GB 0213365.0

<151> 2002-06-11

<150> GB 0300914.9

<151> 2003-01-15

<160> 52

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<213> Streptococcus pneumoniae

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<212> PRT

<213> Streptococcus pneumoniae

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<213> Streptococcus pneumoniae

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<213> Streptococcus pneumoniae

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35 40 45

Asp Gly Asn Trp Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly
50 55 60
Trp Lys Lys Ile Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala
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85 90 95
Ala Lys Glu Gly Ala Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp
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35 40 45
Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp Lys Trp Tyr Tyr
50 55 60
Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val Lys Tyr Lys Asp
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<210> 10
<211> 63
<212> DNA

<213> Streptococcus pneumoniae

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tca 63

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<212> DNA

<213> Streptococcus pneumoniae

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<212> DNA
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<210> 15
<211> 429
<212> DNA
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gtaaaataa 429

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<211> 336
<212> DNA
<213> Streptococcus pneumoniae

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<212> DNA
<213> Homo sapiens

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<210> 18
<211> 1947
<212> DNA
<213> Artificial Sequence

<220>
<223> Hybrid gene between St. pneum. C-LytA, P2 T helper
epitope and human P501S.

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<210> 19
<211> 1662
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimised human P501S

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<212> DNA
<213> Artificial Sequence

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<223> Codon optimised human P501S

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<210> 21
<211> 1688
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimised human P501S

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<210> 22
<211> 1688
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimised human P501S

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cctcgctctt gtggccggctt tccccgtccgc cgcgcggcgc acctgcctgtt ctcattctgt 1140
cgccgtgggtg accgcccacg ccccccgtac cggcttccacc ttcatgtcgc tccagatttc 1200
gccttacacc ctggcgcttc tgcgttccatcg cgagaaggcag gtgttccgtc ccaagtagac 1260

cggggacaca gggggagctt cctctgagga cagcctgatg accagttct tgcccgccc 1320
caagccgggg gccccttcc ccaacggcca tgcggggcg ggcggcagcg gcctgctccc 1380
tccccccccc gccctgtcg ggcctagtgc ctgcgacgtg agcgtgcggg tgggtgggg 1440
ggagccacc gaggctaggg tcgtgcctgg ccggggatc tgcctggacc tggccatcct 1500
cgactccgcc ttccctgtct cccagggtggc gcccagcctg ttcatggca gtatcgtgca 1560
gctgagccag agcgtgaccg cctacatggt gagcggccgc ggcctgggt tggtgccat 1620
ctactttgcc acccaggtcg tttcgacaa gagcgatctc gccaagtata ggcctgact 1680
cgaggcag 1688

<210> 23
<211> 435
<212> DNA
<213> Artificial Sequence

<220>
<223> Hybrid gene between St. pneum. C-LytA, P2 T helper
epitope and a small portion of the 5' end of human
P501S

<400> 23
atggcggccg cttacgtaca ttccgacggc tcttatccaa aagacaagtt tgagaaaatc 60
aatggcaatt ggtactactt tgacagttca ggctatatgc ttgcagaccc ctggaggaag 120
cacacagacg gcaactggta ctggttcgac aactcaggcg aaatggctac aggctggaag 180
aaaatcgctg ataagtggta ctattcaac gaagaagggtg ccatgaagac aggctggtc 240
aagtacaagg acacttggta ctacttagac gctaaagaag ggcgcattgca atacatcaag 300
gctaactcta agttcatgg tatcaactgaa ggcgtcatgg tatcaaattgc ctttatccag 360
tcagcggacg gaacaggctg gtactacctc aaaccagacg gaacactggc agacaggcca 420
gaaaagttca tgtac 435

<210> 24
<211> 435
<212> DNA
<213> Artificial Sequence

<220>
<223> Hybrid gene between St. pneum. C-LytA, P2 T helper
epitope and a small portion of the 5' end of human
P501S - codon-optimised

<400> 24
atggccggccg cttacgtgca tagcgacggg agctacccca aggacaagtt cgagaagatc 60
aacgggacat ggtactactt cgactcctcc ggctacatgc tcggccgaccc ctggcggaag 120
cacaccgacg gcaactggta ctggttcgat aactcgggag agatggccac cggctggaag 180
aagatcgcgg acaagtggta ctattcaac gaggaggcg ccatgaagac cggctgggtg 240

aagtataagg acacctggta ctacctcgac gccaaggagg ggcgcattgca gtatatcaag 300
gccaacagca agttcatcggt catcaccgag ggagtgtatgg tcagcaacgc ctttatccag 360
agcggccacg gcaccggatg gtactacttg aagccggacg gcaccctcgcc ggatcggccc 420
gagaagttca tgtac 435

<210> 25
<211> 435
<212> DNA
<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper epitope and a small portion of the 5' end of human P501S - codon-optimised

<400> 25

atggccgccc cctacgtgca cagcgacggg tcctacccaa aggacaagg tt cgagaagatc 60
aacggcacgt ggtactattt cgacagcagc ggctacatgc tcgcccgtac ctggcgcaag 120
cacaccgacg ggaactggta ctgggtcgac aactctggcg agatggctac ggggtggaaag 180
aagatcgccc acaagtggta ctacttcaac gaggagggcg ccatgaagac cgggtgggtg 240
aagtacaagg acacctggta ctacctggac gctaaggagg ggcgcattca gtacatcaag 300
gcacaactcga agttcatcggt gatcaccgag ggcgtatgg ttagtaacgc tttcatccag 360
agcgcggacg gcacaggctg gtattacctg aagcccgatg gcaccctggc ggacagacct 420
gagaaattca tgtac 435

<210> 26

<211> 464

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper epitope and a small portion of the 5' end of human P501S - codon-optimised

<400> 26

gacggcttagc gccaccatgg ccggccgcta cgtgcatacg gacgggagct accccaagga 60
caagttcgag aagatcaacg ggacatggta ctacttcgac tcctccggct acatgctcg 120
cgaccgctgg cggaaggaca ccgacggcaa ctgggtactgg ttgcataact cgggagagat 180
ggccaccggc tggagaaga tgcggacaa gtgggtactat ttcaacgagg agggcgccat 240
gaagaccggc tgggtgaagt ataaggacac ctgggtactac ctcgacgcac aggagggcgc 300
catcgactat atcaaggcca acagcaagtt catcgacatc accgagggag tgatggtcag 360
caacgccttt atccagagcg ccgacggcac cggatggta tacttgaagc cggacggcac 420
cctcgccgat cggcccgaga agttcatgtt ctgactcgag gcag 464

<210> 27

<211> 652

<212> PRT

<213> Artificial Sequence

<220>

<223> Hybrid protein between St. pneum. C-LytA, P2 T helper epitope and amino acids 51-553 of human P501S

<400> 27

Met	Ala	Ala	Ala	Tyr	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro	Lys	Asp	Lys
1				5			10				15				
Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	Gly	Tyr
							20		25				30		
Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp
							35		40			45			
Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp
						50		55			60				
Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val
						65		70		75			80		
Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met
						85			90			95			

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
 100 105 110
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
 115 120 125
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met
 130 135 140
 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
 145 150 155 160
 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
 165 170 175
 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
 180 185 190
 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro
 195 200 205
 Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp
 210 215 220
 Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp
 225 230 235 240
 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala
 245 250 255
 Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile
 260 265 270
 Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu
 275 280 285
 Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala
 290 295 300
 Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala
 305 310 315 320
 Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg
 325 330 335
 Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His
 340 345 350
 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
 355 360 365
 Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr
 370 375 380
 Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro
 385 390 395 400
 Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
 405 410 415
 Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val
 420 425 430
 Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
 435 440 445
 Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His
 450 455 460
 Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe
 465 470 475 480
 Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg
 485 490 495
 Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala
 500 505 510
 Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro
 515 520 525
 Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu
 530 535 540

Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser
545					550				555					560	
Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly
					565				570					575	
Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu
					580				585					590	
Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser
					595				600					605	
Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val
					610				615					620	
Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala
625					630				635					640	
Lys	Tyr	Ser	Ala	Gly	Gly	His	His	His	His	His	His				
					645				650						

<210> 28
<211> 1959
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding the Hybrid protein between St. pneum.
C-LytA, P2 T helper epitope and amino acids 51-553
of human P501S

<400> 28
atggcggccg cttacgtaca ttccgacggc tcttatccaa aagacaagtt tgagaaaatc 60
aatggcaactt ggtactactt tgacagttaa ggctatatgc ttgcagaccg ctggaggaag 120
cacacagacg gcaactggta ctgggtcgac aactcaggcg aaatggctac aggcttggaa 180
aaaatcgctg ataagtggta ctatttcaac gaagaagggt ccataaagac aggctgggtc 240
aagtacaagg acatTTggta ctacttagac gctaaagaag gcccattgca atacatcaag 300
gctaactcta agttcatgg tatcaactgaa ggcgtcatgg tatcaaatgc ctttatccag 360
tcagcggacg gaacaggctg gtactacctc aaaccagacg gaacactggc agacaggcca 420
gaaaagttca tgtacatggt gctgggcatt ggtccagtgc tgggcttggt ctgtgtcccc 480
ctcttaggtc cagccagtga ccactggcgt ggacgctatg gcccggccg gcccattcattc 540
tggcactgt ctttggcat cctgctgagc ctctttctca tcccaaggggc cggctggcta 600
gcagggctgc tttggccggta tcccaggccc ctggagctgg cactgctcat cctggggctg 660
gggctgtgg acttctgtgg ccaggtgtgc ttcaactccac tggaggccct gctctctgac 720
ctcttccggg accccggacca ctgtcgccag gcctactctg tctatgcctt catgatcagt 780
cttggggctt gcctgggcta cctcctgcct gccattgact gggacaccag tggccctggcc 840
ccctacctgg gcaccccgagga ggagtgcctc tttggcctgc tcaccctcat cttcctcacc 900
tgcgtacgag ccacactgtt ggtggctgag gaggcagcgc tggggccccac cgagccagca 960
gaagggtgtt cggcccccctc cttgtcgccc cactgctgtc catgccccggc cggcttggct 1020
ttccggaaacc tggggccctt gcttccccgg ctgcaccaggc tttgtgtggc catgccccgc 1080
acccttgcgcc ggcttttgtt ggctgagctg tgcagctggta tggactcat gaccttcacg 1140
ctgttttaca cggatttcgtt gggcgagggg ctgttaccagg gcgtgcccag agctgagccg 1200
ggcaccgagg cccggagaca ctatgtgaa ggcgttgcga tggggccctt ggggtgttc 1260
ctgcagtgcg ccatctccctt ggtttctctt ctgttgcattt accggctggc gcagcgattc 1320
ggcactcgag cagtctattt ggccagtgtt gcagcttcc ctgtggctgc cggtgccaca 1380
tgcctgtccc acagtgtggc cgtggtgaca gcttcagccg ccctcacccgg gttcaccttc 1440
tcagccctgc agatcctgcc ctacacactg gcctccctt accaccggga gaagcaggtt 1500
ttctgtccca aataccgggg ggacacttggaa ggtgttagca gtgaggacacg cctgtatgacc 1560
agtttctgc caggccctaa gcctggagct cccttccctt atggacacgt ggggtgtgg 1620
ggcagtggcc tgcctccacc tccacccggc ctctgcgggg ccctctgcctt tgatgtctcc 1680
gtacgtgtgg tgggtgggtga gcccaccggag gccagggtgg ttccggggccg gggcatctgc 1740
ctggacctcg ccatccttggta tagtgccttc ctgtgttccc aggtggccccc atccctgttt 1800

atgggctcca ttgtccagct cagccagtct gtcactgcct atatggtgc tgccgcaggc 1860
ctgggtctgg tcgccattta cttgctaca caggttagtat ttgacaagag cgacttggcc 1920
aaatactcag cgggtgaca ccatcaccat caccattaa 1959

<210> 29
<211> 507
<212> PRT
<213> Artificial Sequence

<220>
<223> Human P501S (amino acids 55-553) fused to 6
histidine residues

<400> 29
Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu
1 5 10 15
Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg
20 25 30
Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu
35 40 45
Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg
50 55 60
Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe
65 70 75 80
Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu
85 90 95
Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe
100 105 110
Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp
115 120 125
Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys
130 135 140
Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr
145 150 155 160
Leu Leu Val Ala Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu
165 170 175
Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala
180 185 190
Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln
195 200 205
Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu
210 215 220
Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp
225 230 235 240
Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly
245 250 255
Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser Leu
260 265 270
Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val Met
275 280 285
Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala Ser
290 295 300
Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His Ser
305 310 315 320
Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe Ser
325 330 335

Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu
 340 345 350
 Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser
 355 360 365
 Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly
 370 375 380

Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
 385 390 395 400
 Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser Val
 405 410 415
 Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly Arg
 420 425 430
 Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu Ser
 435 440 445
 Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser Gln
 450 455 460
 Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val Ala
 465 470 475 480
 Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys
 485 490 495
 Tyr Ser Ala Gly Gly His His His His His His
 500 505

<210> 30
 <211> 1524
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding Human P501S (amino acids 55-553)
 fused to 6 histidine residues

<400> 30
 atggtgctgg gcattggtcc agtgctgggc ctggctgtg tcccgctcct aggctcagcc 60
 agtgaccact ggcgtggacg ctatggccgc cgccggccct tcatactggc actgtccttg 120
 ggcatactgc tgagccttt ttcataccca aggggccggct ggcttagcagg gctgctgtgc 180
 ccgatccca ggccccctgga gctggcactg ctcatacttgg gcgtggggct gctggacttc 240
 tgtggccagg tgcgttccac tccactggag gcccctgtct ctgacacttcc cggggaccgg 300
 gaccactgtc gccaggccta ctctgttat gccttcatga tcagtcttgg gggctgcctg 360
 ggctacctcc tgcctgccat tgactggac accagtgccc tggccccccta cctgggcacc 420
 caggaggagt gcctctttgg cctgctcacc ctcatacttcc tcacctgcgt agcagccaca 480
 ctgtgttgg ctgaggaggc agcgctggc cccacccgagc cagcagaagg gctgtcggcc 540
 ccctccttgt cgccccactg ctgtccatgc cggggccgc tggcttccg gaacctggc 600
 gccctgcttc cccggctgca ccagctgtgc tgccgcattgc cccgcacccct gcgcggctc 660
 ttctgtggctg agctgtgcag ctggatggca ctcatacttcc tcacgtgtt ttacacggat 720
 ttctgtggcg aggggctgtta ccaggcggtg cccagagctg agccgggcac cgaggccgg 780
 agacactatg atgaaggcgt tcggatggc agcctgggc tggatggc gtgcgcattc 840
 tccctggctt tctctcttgtt catggaccgg ctggatggc gattcggcac tcgagcagtc 900
 tatattggcca gtgtggcagc ttccctgtt gctggccgtt ccacatgcct gtcccacagt 960
 gtggccgtgg tgacagcttc agccggccctc accgggttca cttctcagc cctgcagatc 1020
 ctggccctaca cactggcctc cctctaccac cgggagaagc aggtgttccct gcccaaatac 1080
 cgaggggaca ctggagggtgc tagcagttag gacagcctga tgaccagctt cctggccaggc 1140
 cctaaggcctg gagctccctt ccataatggc cacgtgggtg ctggaggcag tggccgtctc 1200
 ccacctccac ccgcgtctg cggggccttgc ctgtgtatc tctccgtacg tggatgggtg 1260

ggtgagccca ccgaggccag ggtggttccg ggccggggca tctgcctgga cctcgccatc 1320
ctggatagtg ctttcctgct gtcccaggta gccccatccc tgtttatggg ctccattgtc 1380
cagctcagcc agtctgtcac tgcctataatg gtgtctgccc caggcctggg tctggtcgcc 1440
atttactttg ctacacaggt agtatttgc aagagcgaact tggccaaata ctcagcgggt 1500
ggacaccatc accatcacca ttaa 1524

<210> 31
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<223> Human P501S (amino acids 1-34 fused to 55-553)
fused to 6 histidine residues

<400> 31
Met Ala Ala Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg
1 5 10 15
Lys Ala Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val
20 25 30
Cys Leu Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp
35 40 45
Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly
50 55 60
Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr
65 70 75 80
Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala
85 90 95
Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp
100 105 110
Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala
115 120 125
Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly
130 135 140
Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp
145 150 155 160
Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe
165 170 175
Met Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val
180 185 190
Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg
195 200 205
Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu
210 215 220
Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp
225 230 235 240
Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu
245 250 255
Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser
260 265 270
Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr
275 280 285
Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala
290 295 300
Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu
305 310 315 320

Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala
 325 330 335
 Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro
 340 345 350
 Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys
 355 360 365
 Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu
 370 375 380
 His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val
 385 390 395 400
 Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr
 405 410 415
 Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu
 420 425 430
 Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly
 435 440 445
 Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu
 450 455 460
 Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu
 465 470 475 480
 Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser
 485 490 495
 His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr
 500 505 510
 Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His
 515 520 525
 Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly
 530 535 540
 Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys
 545 550 555 560
 Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly
 565 570 575
 Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
 580 585 590
 Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro
 595 600 605
 Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu
 610 615 620
 Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu
 625 630 635 640
 Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu
 645 650 655
 Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu
 660 665 670
 Ala Lys Tyr Ser Ala Gly Gly His His His His His His
 675 680 685

<210> 32

<211> 2058

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding Human P501S (amino acids 1-34 fused
to 55-553) fused to 6 histidine residues

<400> 32

atggcggccg tgcagaggct atgggtatcg agactgctaa gacaccgcaa agctcagttg 60
 ttgttggta acttgttgc cttcgggctg gaagtctgtt tggcggccgc ttacgtacat 120
 tccgacggct cttatccaaa agacaaggtt gagaataatca atggcacttg gtactacttt 180
 gacagttcag gctatatgtc tgcatggccg tggaggaagc acacagacgg caactggta 240
 tgggtcgaca actcaggcga aatggctaca ggctgaaaga aaatcgctga taagtggta 300
 tatttcaacg aagaagggtgc catgaagaca ggctgggtca agtacaagga cacttggta 360
 tacttagacg ctaaagaagg cgccatgcaa tacatcaagg ctaactctaa gttcattgg 420
 atcaactgaag gcgtcatggt atcaaatgcc tttatccagt cagcggacgg aacaggctgg 480
 tactaccta aaccagacgg aacactggca gacagggccg aaaagttcat gtacatggta 540
 ctgggcattg gtccagtgct gggctggtc tgggtccgc tcctaggctc agccagtgac 600
 cactggcgtg gacgctatgg ccgcgcggc cccttcatct gggcaactgtc cttgggcata 660
 ctgctgagcc tcttcctcat cccaaggggcc ggctggctag cagggtctgt gtggccggat 720
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<210> 33
 <211> 671
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> St. pneum. C-LytA portion fused to P2 T helper
 epitope fused to Human P501S (amino acids 55-553)
 fused to 6 histidine residues downstream of yeast
 alphapreproto signal sequence

<400> 33

Met	Ala	Ala	Arg	Phe	Pro	Ser	Ile	Phe	Thr	Ala	Val	Leu	Phe	Ala	Ala
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Ser	Ser	Ala	Leu	Ala	Ala	Ala	Tyr	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro
								20				25			30
Lys	Asp	Lys	Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser
								35				40			45
Ser	Gly	Tyr	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn
								50				55			60

Trp Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys
 65 70 75 80
 Ile Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr
 85 90 95
 Gly Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu
 100 105 110
 Gly Ala Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr
 115 120 125
 Glu Gly Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr
 130 135 140
 Gly Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu
 145 150 155 160
 Lys Phe Met Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val
 165 170 175
 Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr
 180 185 190
 Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu
 195 200 205
 Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys
 210 215 220
 Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly Val Gly
 225 230 235 240
 Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu
 245 250 255
 Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser
 260 265 270
 Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu
 275 280 285
 Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr
 290 295 300
 Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys
 305 310 315 320
 Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr
 325 330 335
 Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys
 340 345 350
 Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro
 355 360 365
 Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu
 370 375 380
 Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu
 385 390 395 400
 Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg
 405 410 415
 Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg
 420 425 430
 Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe
 435 440 445
 Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val
 450 455 460
 Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys
 465 470 475 480
 Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly
 485 490 495
 Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu
 500 505 510
 Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr

515	520	525
Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly		
530	535	540
Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly		
545	550	555
Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys		
565	570	575
Asp Val Ser Val Arg Val Val Gly Glu Pro Thr Glu Ala Arg Val		
580	585	590
Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala		
595	600	605
Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val		
610	615	620
Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu		
625	630	635
Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser		
645	650	655
Asp Leu Ala Lys Tyr Ser Ala Gly Gly His His His His His His		
660	665	670

<210> 34
<211> 2477
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding St. pneum. C-LytA portion fused to P2
T helper epitope fused to Human P501S (amino acids
55-553) fused to 6 histidine residues downstream
of yeast alphaprepro signal sequence

<400> 34

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aactggtaat ggttcgacaa ctcaggcgaa atggctacag gctggaaagaa aatcgctgat 180
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gccagtctgt cactgcctat atggtgtctg ccgcaggcct gggcttggtc gccatttact 2400
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atcaccatca ccattaa 2477

<210> 35

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> Human P501S (amino acids 55-553) fused to 6
histidine residues downstream of yeast alphapreproto
signal sequence

<400> 35

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			20					25					30		
Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe	Asp
		35					40					45			
Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu	Phe
		50					55					60			
Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val	Ser
				65			70			75				80	
Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala	Met	Val	Leu	Gly	Ile	Gly	Pro	Val
							85			90			95		
Leu	Gly	Leu	Val	Cys	Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp
							100			105			110		
Arg	Gly	Arg	Tyr	Gly	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu
							115			120			125		
Gly	Ile	Leu	Leu	Ser	Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala
							130			135			140		
Gly	Leu	Leu	Cys	Pro	Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile
							145			150			155		160
Leu	Gly	Val	Gly	Leu	Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro
							165			170			175		
Leu	Glu	Ala	Leu	Leu	Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg
							180			185			190		
Gln	Ala	Tyr	Ser	Val	Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu
							195			200			205		

Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro
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 Tyr Leu Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile
 225 230 235 240
 Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala
 245 250 255
 Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser
 260 265 270
 Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly
 275 280 285
 Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr
 290 295 300
 Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met
 305 310 315 320
 Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln
 325 330 335
 Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp
 340 345 350
 Glu Gly Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile
 355 360 365
 Ser Leu Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly
 370 375 380
 Thr Arg Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala
 385 390 395 400
 Gly Ala Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala
 405 410 415
 Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr
 420 425 430
 Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr
 435 440 445
 Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser
 450 455 460
 Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val
 465 470 475 480
 Gly Ala Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly
 485 490 495
 Ala Ser Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr
 500 505 510
 Glu Ala Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile
 515 520 525
 Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met
 530 535 540
 Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser
 545 550 555 560
 Ala Ala Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val
 565 570 575
 Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala Gly Gly His His His
 580 585 590
 His His His
 595

<210> 36
 <211> 1788

<212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding Human P501S (amino acids 55-553)
 fused to 6 histidine residues downstream of yeast
 alphapreproto signal sequence

<400> 36

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<210> 37
 <211> 1955
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding codon-optimised Human P501S (amino
 acids 51-553) fused to St.pneum. C-LytA P2 helper
 epitope C-LytA

<400> 37

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ccaccggctg gaagaagatc gcggacaagt ggtactattt caacgaggag ggcgcctatga 240
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<210> 38
<211> 2045
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding codon-optimised Human P501S (amino acids 1-553)
fused to St.pneum. C-LytA P2 helper epitope C-LytA

<400> 38
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ccgacccccc ccctctggag ctggccctcc tgatctggg cgtggccctg ctggacttct 780
gcggccagggt gtgtttactt cccttggagg ctctgtctc cgacaccttc cgccgaccccg 840
accactgttag gcaggcttac agcgtgtacg cttcatgtat cagtctgggg ggatgcctgg 900
gctatctgtc gcccgcatac gactgggaca ccagcgccct ggccccctac ctggggactc 960
aggaggaggta cctgttcggc ctgctcacct tgatcttcct gacgtgcgtc gccggccaccc 1020
tgctgggtggc cgaggaggcg gccctggggc ccaccaggacc cgccgaggggc ctgagcgtgc 1080
ccagccttagt ccccccatttc tgccctgtca gggctaggct cgccttcagg aatctggggc 1140

cttgctgcc ccgcctgcat cagctgtgct gtcgcattgcc tcgcacccctg cgccgcctgt 1200
tcgtcgctga gctctttcc tgatggccc tggatgacgtt caccctttc tacaccgact 1260
tcgtggggaa gggcctgtac caggcggtgc ccaggcgca gcccggcacc gaggctaggc 1320
gccattacga cgaggcgctc agatgggtct ctctggctt cttctgtcag tgcccatca 1380
gtctgggttt ctctctgggt atggaccggc tggtgacggtt cttccggcacc cggggcggt 1440
acctcgccctc tgtggcggtt ttccccgtcg ccggccggcgc gacctgcctg tctcattctg 1500
tcgcccgttgtt gaccgcacgc gccgcctgtt ccggcttcac cttcagtgcg ctccagattc 1560
tgccctacac cctggcgctc ctgtaccatc gcgagaagca ggtgttcctg cccaagtacc 1620
gcggggacac agggggagct tcctctgagg acagctgtat gaccagcttc ttgcccggcc 1680
ccaagccggg ggcccctttc cccaacggcc atgtcggggc gggcgccagc ggcctgtcc 1740
ctccccccccc cgccctgtgc ggcgctagtg cctgcgacgt gacgcgtgcgg gtgggtgg 1800
gggagcccac cgaggctagg gtcgtgcctg gccggggat ctgcctggac ctggccatcc 1860
tcgactccgc ctccctgtc tcccaagggtt cggccagctt gttcatgggc agtacgtgc 1920
agctgagcca gagcgtgacc gcctacatgg tgagcggccgc cggctgggg ttgggtggcca 1980
tctactttgc caccctaggc gtgttcgaca agacgatct cgccaagtat agcgcctgag 2040
gatcc 2045

<210> 39
<211> 2105
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding St.pneum. C-LytA P2 helper epitope
C-LytA fused to Human P501S (amino acids 51-553)
fused to Human P501S (amino acids 1-50) -
Codon-optimised

<400> 39
gcggccgcgc caccatggcc gccgcctacg tgcatacgca cggggagctac cccaaggaca 60
agttcgagaa gatcaacggg acatggtaact acttcgactc ctccggctac atgctcgccg 120
accgcgtggcg gaagcacacc gacggcaact ggtactgggtt cgataactcg ggagagatgg 180
ccaccggctg gaagaagatc gcccggcaagt ggtactattt caacggggagg ggcggccatga 240
agaccggctg ggtgaagttt aaggacaccc ggtactaccc cgacggccaaag gaggggcgca 300
tgcagtatata caaggccaac agcaagttca tcggcatcac cggggaggtt atggtcagca 360
acgcctttat ccagagcgcc gacggccaccg gatggtaactt ctgtggcccg gacggccaccc 420
tcgcggatcg gcccggaaa ttcatgtaca tgggtgtggg catcgcccccc gtcctggggcc 480
tcgtgtgtgtt gcccctcttc gggatgtgcgtt ccgcatttttgc gccccggccgc tacggccgccc 540
gcagaccgtt catctggggcc ctgagcctggt gcatcctgtt ctctctcttc ctgatcccccc 600
ggggccggctg gctggccggc ctgctgtgtc ccgcacccccc ccctctggag ctggccctcc 660
tgatccttggg cgtggggctt ctggacttctt gcccggccagggtt gtgttactt cccctggagg 720
ctctgctctc cgaccccttc cgcgacccccc accactgttagt gcaaggcttac agcgtgtacg 780
ccttcattgtat cagttttgggg ggtatgcctgg gctatctgtt gccccgtatc gactgggaca 840
ccagcgccctt gggcccttac ctggggactt aggaggagttt cctgttcggc ctgctcaccc 900
tgatcttcctt gacgtgcgtc gcccggccaccc tggctgggttcc cggggaggccg gcccctggggc 960
ccaccggagcc cggccggggc ctgagcgctc ccagcctgtt gccccatttgc tgccctgtca 1020
gggttaggtt cgccttcagg aatctggggc tttgtgtcc cccgcgttcatc cagctgtgtt 1080
gtcgcatgtt tcgcacccctg cggccgtgtt tcgtcgctgtt gctctgttcc tggatggggcc 1140
tgatgacgtt cacccttttac accggactt tcgtgggggg gggctgtac cagggcggtc 1200
ccaggccgca gcccggccacc gaggctaggc gccattacga cgaggcggtc aggtatgggt 1260
ctctggggctt ctccctgtcag tgcgcattca gtctgggttt ctctctgttcc atggaccggc 1320
tggtgacgtt ctccggacc cggccgtgtt accctgcctc tggccgggtt ttccccgtcg 1380
ccggccggccg gacgtgcctt ttcattttgtt tcgcgtgtt gacgcgttcc gcccctgtca 1440
ccgcgttccatc ctccatgttcc tggccatcac cctggcgctt ctgttaccatc 1500
gcaagggaa ggtgttccctt cccaagttacc gccccggacac agggggaggtt tcctctgttcc 1560
acacgcgttcatc gaccgttcc ttggccggcc ccaaggggggg gggcccttttcc cccaacggcc 1620
atgtcgggggc gggcgccaggc ggcctgttcc ctcccccccccc cggccctgttcc ggcgttcc 1680

cctgcgacgt gacgcgtgcgg gtgggtggg gggagccac cgaggctagg gtcgtgcctg 1740
gccccggat ctgcctggac ctggccatcc tcgactccgc cttcctgctc tcccagggtgg 1800
cgcccagcct gttcatggc agtatcgtgc agctgagcca gagcgtgacc gcctacatgg 1860
tgagcgcgc cggcctgggg ttgggtggca tctactttgc caccagggtc gtgttcgaca 1920
agagcgatct cgccaagtat agcgcctatgg tgcagcggct gtgggtgtcc cggctgctgc 1980
gccatagaaa ggcccagttt ctgctggta acctgtgcac tttcggactg gaggtgtgcc 2040
tggctgcgg gatcacgtac tgccccccc tgctgtgga ggtggcggt gaggagttag 2100
gatcc 2105

<210> 40
<211> 2105
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding Human P501S (amino acids 1-50) fused
to St.pneum. C-LytA P2 helper epitope C-LytA fused
to Human P501S (amino acids 51-553) -
Codon-optimised

<400> 40
gcggccgcgc caccatggtg cagcggctgt ggggtgtccc gctgtgcgc catagaaagg 60
cccagtgtct gctggtaac ctgctgactt tcggactgga ggtgtgcctg gtcgtgcgg 120
tcacgtacgt gccccccctg ctgctggagg tgggcgtgg a g g a g a t g g c c g c c g 180
tgcatacgca cgggagctac cccaaaggaca a g t t c g a g a a g a t c a a c a c g g 240
acttcgactc ctccggctac atgctcgccg accgctggcg a a g a c a c a c c g a c g g c a a c t 300
ggtaactgggt cgataactcg ggagagatgg ccaccggctg a a g a a g a g a t c g c g g a c a a g t 360
ggtaacttattt caacgaggag ggcgcctatga a g a c c g g c t g g t g a a g t a t a a g g a c a c c t 420
ggtaactacctt cgacgcctaa g a g g g c g c c a a g t g c a g t a t a t c a a g g c c a a c a c 480
tcgcatcac cgagggagtg atggtcagca a c g c c t t t a t c a a g g c g c c g a c g g c a c c g 540
gatggtaactt cttgaagccg gacggcaccc tcgcggatcg g c c c g a g a a g a t t c a t g t a c a 600
tggctgtggg catcgcccccc gtcctgggc tcgtgtgtgt g c c c t t c c t c g g a g t g c g t 660
ccgatcattt g c g g g g c c g c a a g t g c a g t a t a t c a a g g c c t t c g a g c c t g g 720
gcattctgtct ctctctttc ctgatcccccc gggccggctg g t g g c c g g c c t g t g t c 780
ccgacccccc cccctctggag ctggccctcc t g a t c t g t g g g c t g g a c t t c t 840
gcggccagggt gtgtttact cccctggagg ctctgtctc c g a c c t t c t c g c g a c c c c g 900
accactgttag gcaggcttac a g c t g t a c g c t t c t g a t c a g t t g g g g g g a t g c c t g g 960
gctatctgtct gcccgcata gactggaca c c a g c g c c t a t g c c t t a c t g g g a c t c 1020
aggaggagtg cctgttcggc ctgctcacct t g a t c t t c t c t g a t g c g c t g g c c a c c c 1080
tgcgtgtggc cgaggaggcg gcctggggc c c a c c g a g c c g c g a g g g c t g a g c g c t c 1140
ccagcctgag cccccatttc t g c c c t g c a g g c t a g g c t c c t t c a g g a t c t g g c g 1200
cttgcgtgcc cccgcctgtcat c a g c t g t g t g t c g c a t g c c t g c a c c c t t g c g c c t g t 1260
tcgtcgctga gctctgttcc t g g a t g g g c c t g a c g t t c a c c c t t c t c a c a c g a c t 1320
tcgtggggga gggctgtac c a g g g c t g c c a c c c g a g g c t g c a c c c t t c a c c c a c c 1380
gccattacga c g a g g g c t c a g g a t g g g c t c t c t g g c a g g a t c t g c c c a t c a 1440
gtctgggttt ctctctggtg a t g g a c c g g c t g g c a g g c t t c c g g c a c c c g g c t g t 1500
acctcgccctc t g t g g c g g c t t t c c t g c a c c c t t c t g c a c c c t t c t g 1560
tcgcccgttgtt g a c c g c c a g c g c t g c a c c c t t c t g c a c c c t t c t g c a c c c t t c 1620
tgccttacac c c t g c g t c t c t g a c c c t t c t g c a c c c t t c t g c a c c c t t c t g c a c c 1680
g c g g g g a c a c a g g g g a g c t t c t g a c c c t t c t g c a c c c t t c t g c a c c c t t c t g c a c c 1740
ccaaaggccgg g g c c c t t t c t c a c c g g c c t t c t g c a c c c t t c t g c a c c c t t c t g c a c c 1800
ctcccccccccc c g c c c t g t g c t c t g a c c c t t c t g c a c c c t t c t g c a c c c t t c t g c a c c 1860
gggagccac c g a g g c t a g g g t c t g c g c t g c a c c c t t c t g c a c c c t t c t g c a c c c t t c t g c a c c 1920
tcgactccgc cttcctgtct t c c c a g g t g g c t g c a c c c t t c t g c a c c c t t c t g c a c c c t t c t g c a c c 1980
agctgagcca g a g c t g a c c c t t c t g c a c c c t t c t g c a c c c t t c t g c a c c c t t c t g c a c c c t t c t g c a c c 2040
tctactttgc c a c c c a g g t c t g c a c a g g c a t c t g c a c c c t t c t g c a c c c t t c t g c a c c c t t c t g c a c c 2100
gatcc 2105

<210> 41
<211> 652
<212> PRT
<213> Artificial Sequence

<220>

<223> St.pneum. C-LytA P2 helper epitope C-Lyta fused to
Human P501S

<400> 41
Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys
1 5 10 15
Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
20 25 30
Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
35 40 45
Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
50 55 60
Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
65 70 75 80
Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
85 90 95
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
100 105 110
Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
115 120 125
Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met
130 135 140
Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
145 150 155 160
Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
165 170 175
Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
180 185 190
Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro
195 200 205
Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp
210 215 220
Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp
225 230 235 240
Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala
245 250 255
Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile
260 265 270
Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu
275 280 285
Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala
290 295 300
Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala
305 310 315 320
Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg
325 330 335
Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His
340 345 350
Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
355 360 365

Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr
370					375							380			
Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro
385					390					395					400
Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser
						405				410					415
Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val
								420		425					430
Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala
								435		440					445
Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His
450						455						460			
Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe
465						470				475					480
Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg
						485				490					495
Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala
						500			505						510
Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro
						515			520			525			
Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu
						530			535			540			
Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser
545							550			555					560
Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly
						565			570						575
Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu
						580			585						590
Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser
						595			600			605			
Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val
						610			615			620			
Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala
625							630			635					640
Lys	Tyr	Ser	Ala	Gly	Gly	His	His	His	His	His	His				
						645				650					

<210> 42
<211> 1959
<212> DNA
<213> Artificial Sequence.

<220>
<223> DNA encoding St.pneum. C-LytA P2 helper epitope
C-LytA fused to Human P501S (plus his tag)

<400> 42
atggcggccg cttacgtaca ttccgacggc tcttatccaa aagacaagtt tgagaaaaatc 60
aatggcactt ggtactactt tgacagttca ggctatatgc ttgcagaccc ctggaggaag 120
cacacagacg gcaactggta ctgggtcgac aactcaggcg aaatggctac aggctggaa 180
aaaatcgctg ataagtggta ctatttcaac gaagaagggtg ccatgaagac aggctgggtc 240
aagtacaagg acacttggta ctacttagac gctaaagaag gcgcctatgca atacatcaag 300
gctaactcta agttcattgg tatcaactgaa ggcgtcatgg tatcaaatgc ctttatccag 360
tcagcggacg gaacaggctg gtactacctc aaaccagacg gaacactggc agacaggcca 420
gaaaagttca tgtacatggt gctggcatt ggtccagtgc tggcctggc ctgtgtcccg 480

ctccttaggt cagccagtga ccactggcgt ggacgctatg gcccgcgcg gcccttcatc 540
 tggcactgt ctttggcat cttgtgagc ctcttctca tcccaaggc cggctggcta 600
 gcaaggctgc tttgtccccgta tcccaggccc ctggagctgg cactgctcat cttggcggtg 660
 gggctgtgg acttctgtgg ccaggtgtgc ttcaactccac tggaggccct gctctctgac 720
 ctcttccggg acccggacca ctgtcgccag gcctactctg tctatgcctt catgatcagt 780
 cttggggct gcctggctta cttcctgcct gccattgact gggacaccag tgccctggcc 840
 ccctacctgg gcacccagga ggagtgcctc tttggctgc tcaccctcat cttcctcacc 900
 tgcgttagcag ccacactgct gttggctgag gaggcagcgc tggggccac cgagccagca 960
 gaagggtgt cggcccccctc ctgtcgccc cactgtgtc catgccggc cggcttggt 1020
 ttccggaaacc tggggccctt gttccccgg ctgcaccagg tttgtgtccg catgccccgc 1080
 accctgcgcc ggctcttcgt ggctgagctg tgcagctgga tggactcat gacccatc 1140
 ctgtttaca cggatttcgt gggcgagggg ctgtaccagg gcgtgcccag agctgagccg 1200
 ggcaccgagg cccggagaca ctatgtgaa ggcgttcgga tgggcagcct ggggtgttc 1260
 ctgcagtgcg ccatctccct ggtttctct ctgtcatgg accggctgtt gcagcgattc 1320
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 tgccctgtccc acagtgtggc cttgtgtgaca gcttcagccg ccctcacccg gttcaccc 1440
 tcagccctgc agatcctgcc ctacacactg gcctccctct accaccgggaa gaagcaggtg 1500
 ttccctggcca aataccgggg ggacactgga ggtgttagca gtgaggacag cctgtatgacc 1560
 agcttcctgc caggccctaa gcctggagct ccctcccta atggacacgt ggggtgtgg 1620
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 atgggctcca ttgtccagct cagccagtc gtcactgcct atatgggtgc tgccgcaggc 1860
 ctgggtctgg tcgcccattta ctttgctaca caggttagtat ttgacaagag cgacttggcc 1920
 aaatactcag cgggtggaca ccatcaccat caccattaa 1959

<210> 43
 <211> 553
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala

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Gln	Leu	Leu	Leu		
Leu	Val	Asn	Leu		
Leu			Thr		
			Phe		
			Gly		
			Leu		
			Glu		
			Val		
			Cys		
			Leu		
20		25	30		
Ala	Ala	Gly	Ile		
Ala	Ala	Thr	Tyr		
		Val	Pro		
		Pro	Pro		
		Leu	Leu		
		Leu	Leu		
		Leu	Glu		
			Val		
35		40	45		
Glu	Glu	Lys	Phe		
Met	Thr	Met	Val		
		Val	Leu		
		Gly	Ile		
		Ile	Gly		
50		55	60		
Leu	Val	Cys	Val		
Leu	Leu	Pro	Leu		
Gly	Ser	Leu	Gly		
Ser	Ala	Ser	Asp		
			His		
			Trp		
			Arg		
65		70	75	80	
Arg	Tyr	Gly	Arg	Arg	
Arg	Arg	Arg	Pro	Phe	
			Ile	Trp	
			Trp	Ala	
			Ala	Leu	
			Ser	Ser	
			Leu	Gly	
85		90		95	
Leu	Leu	Ser	Leu	Phe	
Leu	Ile	Pro	Ile	Leu	
		Arg			
		Ala			
		Gly			
100		105		110	
Leu	Cys	Pro	Asp	Pro	
Pro	Asp	Pro	Arg	Pro	
Leu	Glu	Leu	Leu	Leu	
Leu	Leu	Ala	Leu	Ile	
				Leu	
115		120		125	
Val	Gly	Leu	Leu	Asp	
Leu	Asp	Phe	Cys	Gly	
Leu			Gly	Gln	
			Gly	Val	
130		135		140	
Ala	Leu	Leu	Ser	Asp	
Leu	Phe	Arg	Asp	Pro	
			Asp	His	
			Cys	Arg	
145		150		155	160
Tyr	Ser	Val	Tyr	Ala	
				Phe	
				Met	
				Ile	
165		170		175	
Leu	Leu	Pro	Ala	Ile	
		Asp	Trp	Asp	
			Thr	Ser	
				Ala	
				Leu	
				Ala	
				Pro	
				Tyr	
				Leu	

180	185	190
Gly Thr Gln Glu Glu Cys Leu Phe	Gly Leu Leu Thr Leu Ile Phe Leu	
195	200	205
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu	Glu Ala Ala Leu Gly	
210	215	220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro	Ser Leu Ser Pro His	
225	230	235
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn	Leu Gly Ala Leu	
245	250	255
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro	Arg Thr Leu Arg	
260	265	270
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala	Leu Met Thr Phe	
275	280	285
Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly	Leu Tyr Gln Gly Val	
290	295	300
Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His	Tyr Asp Glu Gly	
305	310	315
Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys	Ala Ile Ser Leu	
325	330	335
Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg	Phe Gly Thr Arg	
340	345	350
Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val	Ala Ala Gly Ala	
355	360	365
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala	Ser Ala Ala Leu	
370	375	380
Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro	Tyr Thr Leu Ala	
385	390	395
Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro	Lys Tyr Arg Gly	
405	410	415
Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met	Thr Ser Phe Leu	
420	425	430
Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly	His Val Gly Ala	
435	440	445
Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys	Gly Ala Ser	
450	455	460
Ala Cys Asp Val Ser Val Arg Val Val Gly Glu Pro	Thr Glu Ala	
465	470	475
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu	Ile Leu Asp	
485	490	495
Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu	Phe Met Gly Ser	
500	505	510
Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met	Val Ser Ala Ala	
515	520	525
Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln	Val Val Phe Asp	
530	535	540
Lys Ser Asp Leu Ala Lys Tyr Ser Ala		
545	550	

<210> 44
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
<223> St.pneum. C-LytA P2 helper epitope C-LytA fused to
Human P501S

<400> 44

Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys
1 5 10 15
Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
20 25 30
Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
35 40 45
Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
50 55 60
Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
65 70 75 80
Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
85 90 95
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
100 105 110
Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
115 120 125
Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met
130 135 140
Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
145 150 155 160
Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
165 170 175
Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
180 185 190
Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro
195 200 205
Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp
210 215 220
Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp
225 230 235 240
Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala
245 250 255
Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile
260 265 270
Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu
275 280 285
Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala
290 295 300
Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala
305 310 315 320
Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg
325 330 335
Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His
340 345 350
Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
355 360 365
Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr
370 375 380
Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro
385 390 395 400
Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
405 410 415
Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val

420	425	430	
Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr	Leu Ala		
435	440	445	
Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys	Leu Ser His		
450	455	460	
Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly	Phe Thr Phe		
465	470	475	480
Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr	His Arg		
485	490	495	
Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly	Gly Ala		
500	505	510	
Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly	Pro Lys Pro		
515	520	525	
Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly	Gly Ser Gly Leu		
530	535	540	
Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val	Ser		
545	550	555	560
Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val	Pro Gly		
565	570	575	
Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe	Leu Leu		
580	585	590	
Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln	Leu Ser		
595	600	605	
Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly	Leu Val		
610	615	620	
Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp	Leu Ala		
625	630	635	640
Lys Tyr Ser Ala			

<210> 45
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
<223> Codon-optimised hybrid protein between St.pneum. C-LytA P2
helper epitope C-LytA fused to Human P501S
amino acids 51-553)

<400> 45			
Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys			
1	5	10	15
Phe Glu Lys Ile Asn Gly Thr Trp Tyr Phe Asp Ser Ser Gly Tyr			
20	25	30	
Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp			
35	40	45	
Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp			
50	55	60	
Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val			
65	70	75	80
Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met			
85	90	95	
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val			
100	105	110	
Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr			

115	120	125
Tyr Leu Lys Pro Asp Gly Thr	Leu Ala Asp Arg	Pro Glu Lys Phe Met
130	135	140
Tyr Met Val Leu Gly Ile Gly	Pro Val Leu Gly	Leu Val Cys Val Pro
145	150	155
Leu Leu Gly Ser Ala Ser Asp His Trp	Arg Arg Gly Arg Tyr Gly	Arg Arg Arg
165	170	175
Arg Pro Phe Ile Trp Ala Leu Ser	Leu Gly Ile Leu Leu	Ser Leu Phe
180	185	190
Leu Ile Pro Arg Ala Gly Trp	Leu Ala Gly Leu Leu	Cys Pro Asp Pro
195	200	205
Arg Pro Leu Glu Leu Ala Leu	Ile Leu Gly Val Gly	Leu Leu Asp
210	215	220
Phe Cys Gly Gln Val Cys Phe	Thr Pro Leu Glu Ala	Leu Leu Ser Asp
225	230	235
Leu Phe Arg Asp Pro Asp His Cys	Arg Gln Ala Tyr Ser Val	Tyr Ala
245	250	255
Phe Met Ile Ser Leu Gly Gly Cys	Leu Gly Tyr Leu Leu	Pro Ala Ile
260	265	270
Asp Trp Asp Thr Ser Ala Leu Ala	Pro Tyr Leu Gly Thr Gln	Glu Glu
275	280	285
Cys Leu Phe Gly Leu Leu Thr	Leu Ile Phe Leu Thr	Cys Val Ala Ala
290	295	300
Thr Leu Leu Val Ala Glu Glu Ala Ala	Leu Gly Pro Thr Glu Pro Ala	
305	310	315
Glu Gly Leu Ser Ala Pro Ser Leu Ser	Pro His Cys Cys Pro Cys	Arg
	325	330
Ala Arg Leu Ala Phe Arg Asn Leu	Gly Ala Leu Leu Pro Arg	Leu His
	340	345
Gln Leu Cys Cys Arg Met Pro Arg	Thr Leu Arg Arg	Leu Phe Val Ala
	355	360
Glu Leu Cys Ser Trp Met Ala Leu Met	Thr Phe Thr Leu Phe Tyr	Thr
	370	375
Asp Phe Val Gly Glu Gly Leu Tyr	Gln Gly Val Pro Arg	Ala Glu Pro
	385	390
Gly Thr Glu Ala Arg Arg His Tyr	Asp Glu Gly Val Arg	Met Gly Ser
	405	410
Leu Gly Leu Phe Leu Gln Cys Ala	Ile Ser Leu Val Phe	Ser Leu Val
	420	425
Met Asp Arg Leu Val Gln Arg Phe	Gly Thr Arg Ala Val	Tyr Leu Ala
	435	440
Ser Val Ala Ala Phe Pro Val	Ala Ala Gly Ala	Thr Cys Leu Ser His
	450	455
Ser Val Ala Val Val Thr Ala Ser	Ala Ala Leu Thr Gly	Phe Thr Phe
	465	470
Ser Ala Leu Gln Ile Leu Pro Tyr	Thr Leu Ala Ser Leu	Tyr His Arg
	485	490
Glu Lys Gln Val Phe Leu Pro Lys	Tyr Arg Gly Asp Thr	Gly Gly Ala
	500	505
Ser Ser Glu Asp Ser Leu Met Thr	Ser Phe Leu Pro Gly	Pro Lys Pro
	515	520
Gly Ala Pro Phe Pro Asn Gly	His Val Gly Ala Gly	Gly Ser Gly Leu
	530	535
Leu Pro Pro Pro Ala Leu Cys Gly	Ala Ser Ala Cys Asp Val	Ser
	545	550
Val Arg Val Val Gly Glu Pro	Thr Glu Ala Arg	Val Val Pro Gly

	565	570	575												
Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu
				580		585							590		
Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser
						595		600				605			
Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val
						610		615			620				
Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala
						625		630		635			640		
Lys	Tyr	Ser	Ala												

<210> 46
<211> 694
<212> PRT
<213> Artificial Sequence

<220>
<223> St.pneum. C-LytA P2 helper epitope C-Lyta fused to
Human P501S (amino acids 1-553)- codon optimised

	<400> 46														
Met	Ala	Ala	Ala	Tyr	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro	Lys	Asp	Lys
						1	5		10			15			
Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	Gly	Tyr
						20		25					30		
Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp
						35		40			45				
Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp
						50		55			60				
Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val
						65		70		75			80		
Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met
						85		90			95				
Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val
						100		105			110				
Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr
						115		120			125				
Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Met	Val	Gln
						130		135			140				
Arg	Leu	Trp	Val	Ser	Arg	Leu	Leu	Arg	His	Arg	Lys	Ala	Gln	Leu	Leu
						145		150		155			160		
Leu	Val	Asn	Leu	Leu	Thr	Phe	Gly	Leu	Glu	Val	Cys	Leu	Ala	Ala	Gly
						165		170			175				
Ile	Thr	Tyr	Val	Pro	Pro	Leu	Leu	Glu	Val	Gly	Val	Glu	Glu	Lys	
						180		185			190				
Phe	Met	Thr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys
						195		200			205				
Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly
						210		215			220				
Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser
						225		230			235			240	
Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro
						245		250			255				
Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Ile	Leu	Gly	Val	Gly	Leu	
						260		265			270				

Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu
 275 280 285
 Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val
 290 295 300
 Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro
 305 310 315 320
 Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln
 325 330 335
 Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val
 340 345 350
 Ala Ala Thr Leu Leu Val Ala Glu Ala Ala Leu Gly Pro Thr Glu
 355 360 365
 Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro
 370 375 380
 Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg
 385 390 395 400
 Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe
 405 410 415
 Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe
 420 425 430
 Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala
 435 440 445
 Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met
 450 455 460
 Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser
 465 470 475 480
 Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr
 485 490 495
 Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu
 500 505 510
 Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe
 515 520 525
 Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr
 530 535 540
 His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly
 545 550 555 560
 Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro
 565 570 575
 Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Ser
 580 585 590
 Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp
 595 600 605
 Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val
 610 615 620
 Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe
 625 630 635 640
 Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln
 645 650 655
 Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly
 660 665 670
 Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp
 675 680 685
 Leu Ala Lys Tyr Ser Ala
 690

<211> 694
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> St.pneum. C-LytA P2 helper epitope C-Lyta fused to
 Human P501S (amino acids 51-553) fused to Human
 P501S (amino acids 1-50) - codon-optimised

 <400> 47
 Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys
 1 5 10 15
 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
 20 25 30
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
 35 40 45
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
 50 55 60
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
 65 70 75 80
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
 85 90 95
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
 100 105 110
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
 115 120 125
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met
 130 135 140
 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
 145 150 155 160
 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
 165 170 175
 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
 180 185 190
 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro
 195 200 205
 Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp
 210 215 220
 Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp
 225 230 235 240
 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala
 245 250 255
 Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile
 260 265 270
 Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu
 275 280 285
 Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala
 290 295 300
 Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala
 305 310 315 320
 Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg
 325 330 335
 Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His
 340 345 350
 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
 355 360 365
 Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr

370	375	380
Asp Phe Val Gly Glu	Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro	
385	390	395 400
Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser		
	405	410 415
Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val		
	420	425 430
Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala		
	435	440 445
Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His		
	450	455 460
Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe		
	465	470 475 480
Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg		
	485	490 495
Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala		
	500	505 510
Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro		
	515	520 525
Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu		
	530	535 540
Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser		
	545	550 555 560
Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly		
	565	570 575
Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu		
	580	585 590
Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser		
	595	600 605
Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val		
	610	615 620
Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala		
	625	630 635 640
Lys Tyr Ser Ala Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg		
	645	650 655
His Arg Lys Ala Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu		
	660	665 670
Glu Val Cys Leu Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu		
	675	680 685
Glu Val Gly Val Glu Glu		
	690	

<210> 48
<211> 694
<212> PRT
<213> Artificial Sequence

<220>
<223> Human P501S (amino acids 1-50) fused to St.pneum.
C-LytA P2 helper epitope C-Lyta fused to Human
P501S (amino acids 51-553) - codon optimised

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<400> 48
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
      1           5           10          15

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Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
20 25 30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
35 40 45
Glu Glu Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys
50 55 60
Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser
65 70 75 80
Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp
85 90 95
Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile
100 105 110
Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly
115 120 125
Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly
130 135 140
Ala Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
145 150 155 160
Gly Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly
165 170 175
Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys
180 185 190
Phe Met Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys
195 200 205
Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly
210 215 220
Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser
225 230 235 240
Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro
245 250 255
Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu
260 265 270
Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu
275 280 285
Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val
290 295 300
Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro
305 310 315 320
Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln
325 330 335
Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val
340 345 350
Ala Ala Thr Leu Leu Val Ala Glu Ala Ala Leu Gly Pro Thr Glu
355 360 365
Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro
370 375 380
Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg
385 390 395 400
Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe
405 410 415
Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe
420 425 430
Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala
435 440 445
Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met
450 455 460
Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser

465	470	475	480
Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr			
485	490	495	
Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu			
500	505	510	
Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe			
515	520	525	
Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr			
530	535	540	
His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly			
545	550	555	560
Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro			
565	570	575	
Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser			
580	585	590	
Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp			
595	600	605	
Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val			
610	615	620	
Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe			
625	630	635	640
Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln			
645	650	655	
Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly			
660	665	670	
Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp			
675	680	685	
Leu Ala Lys Tyr Ser Ala			
690			

<210> 49

<211> 1971

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding Human MUC-1 fused to St.pneum. C-LytA
P2 helper epitope C-LytA

<400> 49

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gttacagggtt ctggcatgc aagctctacc ccaggtggag aaaaggagac ttccggctacc 120
cagagaagtt cagtgcggcag ctctactgag aagaatgctg ttagtatgac cagcagcgta 180
ctctccagcc acagccccgg ttcaggctcc tccaccactc agggacagga tgtcactctg 240
gccccggcca cggAACCCAGC ttcaggttca gctgccacct ggggacagga tgtcacctcg 300
gtcccagtca ccaggccagc cctgggctcc accaccccgc cagccacgca tgtcacctca 360
gccccggaca acaaggccagc cccgggctcc accgccccccc cagccacgg tgtcacctcg 420
gccccggaca ccaggccgccc cccgggctcc accgccccccc cagccacgg tgtcacctcg 480
gccccggaca ccaggccgccc cccgggctcc accgccccccc cagccacgg tgtcacctcg 540
gccccggaca ccaggccggc cccgggctcc accgccccccc cagcccatgg tgtcacctcg 600
gccccggaca acaggcccgc ctggcgtcc accgccccctc cagttccacaa tgtcacctcg 660
gcctcaggct ctgcattcagg ctcagcttct actctgggtgc acaacggcac ctctgccagg 720
gctaccacaa ccccagccag caagagcact ccattctcaa ttcccagcca ccactctgat 780
actccttacca cccttggccag ccatagcacc aagactgtatg ccagtagcac tcaccatagc 840
acggtaacctc ctctcacctc ctccaaatcac agcacttctc cccagttgtc tactgggtc 900

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tctttcttt tcctgtctt tcacattca aacccagg ttaattcctc tctgaaat 960
cccagcaccc actactacca agagctgcag agagacattt ctgaaatgtt tttgcagatt 1020
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gtacaattga ctctggcctt ccgagaagg accatcaatg tccacgacgt ggagacacag 1140
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<210> 50
<211> 656
<212> PRT
<213> Artificial Sequence

<220>
<223> Human MUC-1 fused to St.pneum. C-LytA P2 helper
epitope C-LytA

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Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
50 55 60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65 70 75 80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
85 90 95
Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
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Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
115 120 125
Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
130 135 140
Arg Pro Pro Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
145 150 155 160
Ala Pro Asp Thr Arg Pro Pro Pro Gly Ser Thr Ala Pro Ala Ala His
165 170 175
Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
180 185 190
Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu
195 200 205
Ala Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser
210 215 220

Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg
 225 230 235 240
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 His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
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 Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
 275 280 285
 Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
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 Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp
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 Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met
 325 330 335
 Phe Leu Gln Ile Tyr Lys Gln Gly Phe Leu Gly Leu Ser Asn Ile
 340 345 350
 Lys Phe Arg Pro Gly Ser Val Val Gln Leu Thr Leu Ala Phe Arg
 355 360 365
 Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr
 370 375 380
 Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser
 385 390 395 400
 Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val
 405 410 415
 Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala
 420 425 430
 Leu Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg
 435 440 445
 Lys Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His
 450 455 460
 Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Arg Tyr Val Pro
 465 470 475 480
 Pro Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn
 485 490 495
 Gly Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser
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 Ala Asn Leu Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro
 515 520 525
 Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser
 530 535 540
 Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn
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 Trp Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys
 565 570 575
 Ile Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr
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 Gly Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu
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 Gly Ala Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr
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 Glu Gly Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr
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 Gly Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu
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<211> 2037
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding St.pneum. C-LytA P2 helper epitope
 C-LytA fused to Human MUC-1

<400> 51

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<210> 52
 <211> 678
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> St.pneum. C-LytA P2 helper epitope C-LytA fused
 to Human MUC-1

<400> 52

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Trp	Lys	Lys	Ile	Ala	Asp	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala
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		165						170					175		
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		210					215					220			
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Val	Thr	Leu	Ala	Pro	Ala	Thr	Glu	Pro	Ala	Ser	Gly	Ser	Ala	Ala	Thr
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Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile
485 490 495
Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu
500 505 510
Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu
515 520 525
Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe
530 535 540
Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser
545 550 555 560
Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly
565 570 575
Ala Gly Val Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val
580 585 590
Leu Val Ala Leu Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln
595 600 605
Cys Arg Arg Lys Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp
610 615 620
Thr Tyr His Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg
625 630 635 640
Tyr Val Pro Pro Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser
645 650 655
Ala Gly Asn Gly Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala
660 665 670
Ala Thr Ser Ala Asn Leu
675